



RESULT 2  
 ID Y021-SYNY3 STANDARD: PRT; 277 AA.  
 AC 055682;  
 DT 01-NOV-1997 (REL. 35, CREATED)  
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)  
 DE PUTATIVE PROTEASE SLR021 (EC 3.4.-.-).  
 GN SLR021.  
 OS SYNECHOCYSTIS SP. (STRAIN PCC 6803).  
 OC BACTERIA; CYANOBACTERIA; CHROCCALES; SYNECHOCYSTIS.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 96127529.  
 RA KANERU T., TANAKA A., SATO S., KOTANI H., SAZUKA T., MIYAIMA N.,  
 RA SUGIURA M., TABATA S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 Synchocystis sp. strain PCC6803. I. Sequence features in the 1 Mb  
 region from map positions 648 to 928 of the genome.";  
 RT DNA RES. 2:155-166(1995).  
 RL 2:155-166(1995).  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY U7.  
 CC  
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 CC  
 CC  
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 CC  
 DR EMBL; D64000; G101581; -.  
 DR PFAM; PF01343; Peptidase\_U7; 1.  
 KW HYPOTHETICAL PROTEIN; HYDROLASE; PROTEASE.  
 SQ SEQUENCE 277 AA; 30274 MW; E996320D CRC32;

Query Match 15.7%; Score 94; DB 1; Length 277;  
 Best Local Similarity 39.4%; Pred. No. 3 43e-01;  
 Matches 13; Conservative 9; Mismatches 10; Indels 1; Gaps 1;  
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 CC  
 CC  
 DR EMBL; D64000; G101581; -.  
 DR PFAM; PF01343; Peptidase\_U7; 1.  
 KW HYPOTHETICAL PROTEIN; HYDROLASE; PROTEASE.  
 SQ SEQUENCE 277 AA; 30274 MW; E996320D CRC32;

Query Match 15.7%; Score 94; DB 1; Length 364;  
 Best Local Similarity 39.4%; Pred. No. 3 43e-01;  
 Matches 13; Conservative 10; Mismatches 11; Indels 2; Gaps 2;  
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 CC  
 CC  
 DR EMBL; D64000; G101581; -.  
 DR PFAM; PF01343; Peptidase\_U7; 1.  
 KW HYPOTHETICAL PROTEIN; HYDROLASE; PROTEASE.  
 SQ SEQUENCE 364 AA; 41110 MW; DA776C59 CRC32;

Query Match 15.7%; Score 94; DB 1; Length 364;  
 Best Local Similarity 39.4%; Pred. No. 3 43e-01;  
 Matches 13; Conservative 10; Mismatches 11; Indels 2; Gaps 2;  
 CC modified and this statement is not removed. Usage by and for commercial  
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 or send an email to license@isb-sib.ch).  
 CC  
 CC  
 DR EMBL; D64000; G101581; -.  
 DR PFAM; PF01343; Peptidase\_U7; 1.  
 KW HYPOTHETICAL PROTEIN; HYDROLASE; PROTEASE.  
 SQ SEQUENCE 364 AA; 41110 MW; DA776C59 CRC32;

RESULT 3  
 ID YB88\_ECOLI STANDARD: PRT; 364 AA.  
 AC P33667; P77709;  
 DT 01-FEB-1994 (REL. 28, CREATED)  
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)  
 DE HYPOTHETICAL 41.1 KD PROTEIN IN RHSD-GCL INTERGENIC REGION.  
 GN YBB.  
 OS ESCHERICHIA COLI.  
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIAEAE;  
 OC ESCHERICHIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP STRAIN-K12 / MG1655;  
 RX MEDLINE; 97426617.  
 RA BLAYTON F.R., PLUNKETT G. III, BLOCH C.A., PERNIA N.T., BURLAND V.,  
 RA RILEY M., COLLADO-VIDEZ J., GLASNER J. D., RODE C.K., MAYHEW G.F.,  
 RA GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,  
 RA MAU B., SHAO Y.;  
 RA "The complete genome sequence of Escherichia coli K-12.";  
 RL SCIENCE 277:1453-1474(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655;  
 RA ROBERTS D., ALLEN E., ARAUJO R., APARICIO A., CHUNG E., DAVIS K.,  
 RA DUNCAN M., FEDERSPIEL N., HYMAN R., KALMAN S., KOMP C., KURDI O.,  
 RA LEW H., LIN D., NAMATH A., OFFNER P., SCHRAMM S., DAVIS R.W.;  
 RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDJB DATA BANKS.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655;  
 RA ROBERTS D., ALLEN E., ARAUJO R., APARICIO A., CHUNG E., DAVIS K.,  
 RA DUNCAN M., FEDERSPIEL N., HYMAN R., KALMAN S., KOMP C., KURDI O.,  
 RA LEW H., LIN D., NAMATH A., OFFNER P., SCHRAMM S., DAVIS R.W.;  
 RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDJB DATA BANKS.  
 RN  
 RP SEQUENCE .OF 268-364 FROM N.A.

RESULT 4  
 ID SYAC\_YEAST STANDARD: PRT; 958 AA.  
 AC P40825;  
 DT 01-FEB-1995 (REL. 31, CREATED)  
 DT 01-OCT-1995 (REL. 34, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE ALANYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.7) (ALANINE--T RNA  
 DE LIGASE) (ALARS).  
 GN ALA1 OR YOR35C.  
 OS SACCHAROMYCES CERVISIAE (BAKER'S YEAST).  
 OC EUKARYOTA; FUNGI; ASCOMYCETES; SACCHAROMYCETES;  
 OC SACCHAROMYCETACEAE; SACCHAROMYCES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP RIMASTER T.L., SCHIMMEL P.;  
 RL SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDJB DATA BANKS.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 97051585.  
 RA PARLE-KODNER A.G., HAND N.J., GOULDING S.G., WOLFE K.H.;  
 RT Sequence of 29 kb around the PDR10 locus on the right arm of  
 RT Saccharomyces cerevisiae chromosome XV: similarity to part of  
 RT chromosome I.";  
 RL YEAST 12:999-1004(1996).  
 CC -!- CATALYTIC ACTIVITY: ATP + L-ALANINE + TRNA(ALA) = AMP +  
 CC PYROPHOSPHATE + L-ALANYL-TRNA(ALA).  
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.  
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 or send an email to license@isb-sib.ch).  
 CC  
 DR EMBL; U18672; G69338; -.  
 DR EMBL; Z49821; E228690; -.  
 DR EMBL; Z75243; E222159; -.  
 DR SGD; L000257; ALA1  
 PROSITE; PS00179; AA\_TRNA\_LIGASE\_II\_1; FALSE\_NEG.



FT	DOMAIN	366	389	GLU/GLN-RICH.	Best Local Similarity 34.2%; Pred. No. 1.52e+00;
FT	VARIANT	382	385	MISSING (IN SOME STRAINS).	Matches 13; Conservative 11; Mismatches 12; Indels 2; Gaps 2;
FT	CONFLICT	15	15	MISSING (IN REF. 1).	
FT	CONFLICT	63	63	Q -> K (IN REF. 1).	
FT	CONFLICT	207	207	E -> R (IN REF. 1).	
FT	CONFLICT	288	S -> A (IN REF. 1).		
FT	CONFLICT	294	RO -> KA (IN REF. 1).		
FT	CONFLICT	315	316	NK -> GG (IN REF. 1).	
SQ	SEQUENCE	395	AA:	45029 MW: 3B5145BD CRC32;	
Query Match Score 89; DB 1; Length 395; Best Local Similarity 31.5%; Pred. No. 1.52e+00; Matches 23; Conservative 20; Mismatches 27; Indels 3; Gaps 3;					
Db	322	LEQFQQLGNSGEVSHLSFLEKSLREKINNSFMSTLEKKGSPDPOQAL-PLP-EQAQEQ	379	Db 7 URLIFGSGHERDKRNLTINAVNAOE-SWVILPQEE 43	
Qy	4	LEELRLVFGPLGDLQHQLRDTSSSSDELSSWILLEKUGMAFQ-EALDQGPEDQGSPF	62	Qy 7 LRLVFGPLGDLQHQLRDTSSSSDELSSWILLEKUGMAFQ-EALDQGPEDQGSPF 43	
Db	380	AQEQQEQVQPKP	392		
Qy	63	AQELDDGQOASP	75		
RESULT 7					
ID	SECA_TREPA	STANDARD:	PRT:	916 AA.	
AC	083394;				
DT	15-DEC-1998 (REL. 37, CREATED)				
DT	15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)				
DE	PREPROTEIN TRANSLOCASE SEC4 SUBUNIT.				
DE	SEC4A OR TPO379.				
GN					
OS					
OC					
OC					
RN					
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 98332770.				
RA	FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,				
RA	DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,				
RA	SODERQREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,				
RA	HALAK H., RICHARDSON D., HOWELL J.R., CHIDAMBARAM M., UTTERBACK T.,				
RA	MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,				
RA	HATCH B., HORST K., ROBERTS K., WATHEY L., WEIDMAN J., SMITH H.O.,				
RA	VENTER J.C.;				
RT	"Complete genome sequence of treponema pallidum, the syphilis				
RT	spirochete.", SCIENCE 281:375-388(1998).				
RL	-1- FUNCTION: INVOLVED IN PROTEIN EXPORT. INTERACTS WITH THE SECY/SEC60				
CC	SUBUNITS. SEC60 HAS A CENTRAL ROLE IN COUPLING THE HYDROLYSIS OF				
CC	ATP TO THE TRANSFER OF PRE-SECRETORY PERPLASMIC AND OUTER				
CC	MEMBRANE PROTEINS ACROSS THE MEMBRANE (BY SIMILARITY).				
CC	-1- SUBUNIT: ONE OF SEVEN SECRETORY PROTEINS (SEC60 & SECY) THAT				
CC	COMprise THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS				
CC	(BY SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF PLASMA MEMBRANE				
CC	(BY SIMILARITY).				
CC	-1- SIMILARITY: BELONGS TO THE SEC60 FAMILY.				
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CC	DR: EMBL: L15923; G299675; -				
CC	DR: EMBL: Z72947; E243549; -				
CC	DR: SGD: L0002309; TI4631.				
CC	DR: PIR: A48086; A48086.				
CC	DR: PROSITE: PS00030; RNP_1; FALSE_NEG.				
CC	DR: KW INITIATION FACTOR; PROTEIN BIOSYNTHESIS; RNA-BINDING;				
CC	KW MULTIGENE FAMILY.				
FT	DOMAIN 173 200 PRO/SER/THR-RICH.				
FT	DOMAIN 375 384 ALA/GLU/RICH.				
FT	DOMAIN 488 553 ARG/SER-RICH.				
FT	DOMAIN 873 899 ARG/SER-RICH.				
FT	DOMAIN 869 872 POLY-GLU.				
FT	DOMAIN 647 652 RNA-BINDING (RNP2) (BY SIMILARITY).				
FT	DOMAIN 742 749 RNA-BINDING (RNP1) (BY SIMILARITY).				
FT	CONFFLICT 7 7 H -> Q (IN REF. 1).				
FT	CONFFLICT 37 37 T -> N (IN REF. 1).				
FT	CONFFLICT 110 110 Q -> K (IN REF. 1).				
FT	CONFFLICT 207 207 R -> K (IN REF. 1).				
FT	CONFFLICT 361 361 D -> E (IN REF. 1).				
SQ	SEQUENCE 952 AA; 107101 MW; DEB23E89 CRC32;				
Query Match. Score 89; DB 1; Length 916;					
14.9%;					



RT causing hereditary elliptocytosis";  
 RL J. CLIN. INVEST. 84:1243-1252(1989).  
 RN [3]  
 SEQUENCE OF 7-601.  
 RP MEDLINE; 84087888.  
 RT "Structure of human erythrocyte spectrin. II. The sequence of the alpha-I domain.",  
 RT alpha-I domain.",  
 RT SPEICHER D.W., DAVIS G., MARCHESSI V.T.;  
 RA J. BIOL. CHEM. 258:14938-14947(1983).  
 RP SEQUENCE OF 7-125.  
 RX SPEICHER D.W., DAVIS G., YURCHENCO P.D., MARCHESSI V.T.;  
 RA "Structure of human erythrocyte spectrin. I. Isolation of the alpha-I domain and its cyanothen bromide peptides.",  
 RL J. BIOL. CHEM. 258:14931-14937(1983).  
 RN [5]  
 RP SEQUENCE OF 320-450 FROM N.A.  
 RX MEDLINE; 86205962.  
 RA LINNENBACH A.J., SPEICHER D.W., MARCHESSI V.T., FORGET B.G.;  
 RT "Cloning of a portion of the chromosomal gene for human erythrocyte alpha-spectrin by using a synthetic gene fragment.",  
 RL PROC. NATL. ACAD. SCI. U.S.A. 83:2397-2401(1986).  
 RN [6]  
 RP SEQUENCE OF 7-533 FROM N.A., AND VARIANT PRO-260; PRO-261 AND PRO-471.  
 RX MEDLINE; 9009318.  
 RA SAHR K.E., TOBE T., SCARPA A.L., LAUGHTINGHOUSE K., MARCHESSI S.L.,  
 RA AGRE P., LINNENBACH A.J., MARCHESSI V.T., FORGET B.G.;  
 RT "Sequence and exon-intron organization of the DNA encoding the alpha I domain of human spectrin. Application to the study of mutations causing hereditary elliptocytosis";  
 RT J. CLIN. INVEST. 84:1243-1252(1989).  
 RN [7]  
 RP PARTIAL SEQUENCE.  
 MEDLINE; 84295638.  
 RA SPEICHER D.W., MARCHESSI V.T.;  
 RT "Erythrocyte spectrin is comprised of many homologous triple helical segments";  
 RT NATURE 311:177-180(1984).  
 RL [8]  
 RP IDENTIFICATION OF PROBABLE FRAMESHIFT IN 2407-2418.  
 RA GIBSON T.J.;  
 RL UNPUBLISHED OBSERVATIONS (MAR-1995).  
 RN [9]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE; 97001215.  
 RA MATILET P., ALLOISIO N., MORLE L., DELAUNAY J.;  
 RT "Spectrin mutations in hereditary elliptocytosis and hereditary spherocytosis";  
 RL HUM. MUTAT. 8:97-107(1996).  
 RN [10]  
 RP VARIANT SER-24.  
 MEDLINE; 94289716.  
 RX PARQUET N., DEVAUX I., BOUTANGER L., GALAND C., BOIVIN P.,  
 RA LECOMTE M.-C., DHERMY D., GABARZ M.;  
 RT "Identification of three novel spectrin alpha I/74 mutations in hereditary elliptocytosis: further support for a triple-stranded folding unit model of the spectrin heterodimer contact site.",  
 RL BLOOD 84:303-308(1994).  
 RN [11]  
 RP VARIANTS CYS-28, HIS-28, LEU-28 AND SER-28.  
 MEDLINE; 91358728.  
 RA COETZER T.L., SAHR K., PRCHAL J., BLACKLOCK H., PETERSON L., KOLER R.,  
 RA DOYLE J., MANASTER J., PALEK J.;  
 RT "Four different mutations in codon 28 of alpha spectrin are associated with structurally and functionally abnormal spectrin alpha I/74 in hereditary elliptocytosis";  
 RT J. CLIN. INVEST. 88:743-749(1991).  
 RN [12]  
 RP VARIANTS SER-28 AND ARG-48.  
 MEDLINE; 9134849.  
 RA FLOYD P.B., GALLAGHER P.G., VALENTINO L.A., DAVIS M., MARCHESSI S.L.,  
 RA ~~FORGET~~ B.G.;  
 RN [13]  
 RP VARIANT SER-45.  
 RX MEDLINE; 89323459.  
 RA LECOMTE M.-C., GRANDCHAMP B., FEO C., GAUTIERO H.,  
 RA DEVAUX I., BOURNIER M., GRANDCHAMP B., FEO C., GAUTIERO H.,  
 RA SAHR K.E., FORGET B.G., BOIVIN P., DHERMY D.;  
 RT "Sp alpha I/78: a mutation of the alpha I spectrin domain in a white kindred with HE and HPP phenotypes.",  
 RL BLOOD 74:1126-1133(1989).  
 RN [14]  
 RP VARIANT PRO-207.  
 RX MEDLINE; 92176375.  
 RA GAULAGER P.G., TSE W.T., COETZER T., LECOMTE M.-C., GABARZ M.,  
 RA ZARKOWSKY H.S., BARUCHEL A., BALLAS S.K., DHERMY D., PALEK J.,  
 RA FORGET B.G.;  
 RT "A common type of the spectrin alpha I 46-50a-kD peptide abnormality in hereditary elliptocytosis and propoikilocytosis is associated with a mutation distant from the proteolytic cleavage site. Evidence for the functional importance of the triple helical model of spectrin.",  
 RT J. CLIN. INVEST. 89:892-898(1992).  
 RN [15]  
 RP VARIANT VAL-1857.  
 RX MEDLINE; 92253053.  
 RA WILMOTTE R., MARCHEL J., MORLE L., BAKLOUTI F., PHILIPPE N.,  
 RA KASTALY R., KOTIJA L., DELAUNAY J., ALLOISIO N.;  
 RT "Low expression allele alpha I/50 of red cell spectrin is associated with mutations in exon 40 (alpha V/41 polymorphism) and intron 45 and with partial skipping of exon 46.",  
 RT J. CLIN. INVEST. 91:2091-2096(1993).  
 RN [16]  
 RP VARIANT BARCELONA.  
 RX MEDLINE; 9372367.  
 RA DALLA VENEZIA N., ALLOISIO N., FORISSIER A., DENOROY L., AYMERICH M.,  
 RA VIVES-CORRENS J.L., BESALUCH J., BESALUCH J.;  
 RT "Ellipoikilocytosis associated with the alpha I/50-46b)",  
 RT mutation in spectrin Barcelona (alpha I/50-46b).",  
 RL BLOOD 82:1661-1665(1993).  
 RN [17]  
 RP VARIANT CAGLIARI.  
 RX MEDLINE; 9443025.  
 RA SAHR K.E., COETZER T.L., MOY L.S., DERICK L.H., CHISHTI A.H.,  
 RA JAROLIM P., LORENZO F., MIRAGLIA DEL GIUDICE E., TOLASCON A.,  
 RA GALLANELLO R.;  
 RT "Spectrin Cagliari: an Ala-->Gly substitution in helix 1 of beta spectrin repeat 17 that severely disrupts the structure and self-association of the erythrocyte spectrin heterodimer.",  
 RT J. BIOL. CHEM. 268:22656-22662(1993).  
 RN [18]  
 RP VARIANT CULOZ AND LYON.  
 RX MEDLINE; 90347052.  
 RA MORLE L., ROUX A.-F., ALLOISIO N., POTHIER B., STARCK J., DENOROY J.,  
 RA MORLE F., RODIGZ R.C., FORGET B.G., DELAUNAY J., GODER J.;  
 RT "Two elliptocytogenic alpha I/74 variants of the spectrin alpha I domain. Spectrin Culoz (Gly-->CPT; alpha I 40 GLY-->Val) and spectrin Lyon (CCT-->TTT; alpha I 43 Leu-->Phe).",  
 RT J. CLIN. INVEST. 86:548-554(1990).  
 RN [19]  
 RP VARIANT JENDOUBA.  
 RX MEDLINE; 92245619.  
 RA ALLOISIO N., WILMOTTE R., MORLE L., BAKLOUTI F., MARCHEL J.,  
 RA DUCLUZEAU M.-T., DENOROY L., FEO C., FORGET B.G., KASTALY R.,  
 RA DELAUNAY J.;  
 RT "Spectrin Jendouba: an alpha II/31 spectrin variant that is associated with elliptocytosis and carries a mutation distant from the dimer self-association site.",  
 RT BLOOD 80:809-815(1992).  
 RN [20]

RA RX VARIANT TUNIS

RA MEDLINE: 89321436.

RA MORLE L., MORLE F., ROUX A.-F., GODET J., FORGET B.G., DENOROY L.,

RA GARBARZ M., DHERMY D., KASFALLY R., DELAUNAY J.; DELAUNAY, J.; DELAUNAY, J.

RA "Spectrin TUNIS (SP alpha 1/78), an elliptocytogenic variant, is due

RT to the CCG->TGG codon change (Arg->Trp) at position 35 of the

RT alpha 1 domain";

RT BLOOD 74:820-832(1989).

RN [21]

RA VARIANT GENOVA.

RA MEDLINE: 94250920.

RA PERROTTA S., DEL GIUDICE E.M., ALLOISIO N., SCIARRATTA G., PINTO L.,

RA DELAUNAY J., CUTILLO S., LOLASCON A.; LOLASCON, A.

RT "Mild elliptocytosis associated with the alpha 34 Arg->Trp mutation

RT in spectrin Genova (alpha 1/74).";

RL BLOOD 83:3346-3349(1994).

RN [22]

RA VARIANT ANASTASIA.

RA MEDLINE: 92290423.

RA PERROTTA S., LOLASCON A., DE ANGELIS F., PAGANO L., COLOMNA G.,

RA CUTILLO S., DEL GIUDICE E.M.;

RT "Spectrin Anastasia (alpha 1/78): a new spectrin variant (alpha 45

RT Arg->Thr) with moderate elliptocytogenic potential.;"

RL J. HAEMATOL. 89:933-937(1995).

RN [23]

RA -!- FUNCTION: SPECTRIN IS THE MAJOR CONSTITUENT OF THE CYTOSKELETAL

RA NETWORK UNDERLYING THE ERYTHROCYTE PLASMA MEMBRANE. IT ASSOCIATES

RA WITH BAND 4.1 AND ACTIN TO FORM THE CYTOSKELETAL SUPERSTRUCTURE OF

RA THE ERYTHROCYTE PLASMA MEMBRANE.

Note: remainder of annotations omitted.

Query Match

Best Local Similarity 14.7%; Score 88; DB 1; Length 2418;

Matches 15; Conservative 15; Mismatches 15; Indels 3; Gaps 3;

Db 1318 AEDLTGIEILLERH-QHRADMEEAPTFFQALEDSFAELLDGHHASP 1364

Qy 30 SDELWSIELLEKDGMAFOEALDP-GP-FDQGSPFAQELLDGQQASP 75

RESULT 12

ID YDJA\_ECOLI STANDARD; PRT; 183 AA.

ID P24250; CREATED)

DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)

DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE HYPOTHETICAL 20.1 KD PROTEIN IN SELD-SPPA INTERGENIC REGION (ORF183).

GN YDJA

OS ESCHERICHIA COLI.

OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIAE;

OC ESCHERICHIA.

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE: 9313715.

RA SAWERS G., HEIDER J., ZEEHEIN E., BOECK A.;

RA "Expression and operon structure of the sel genes of Escherichia coli

RT and identification of a third selenium-containing formate

RT dehydrogenase isoenzyme.;"

RL J. BACTERIOL. 173:4983-4993(1991).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-K12 / MG1655;

RA MEDLINE: 9742617.

RA BLATTNER F.R., PUNKETT G. III, BLOCH C.A., PERNIA N.T., BURLAND V.,

RA RILEY M., COLLADO-VIDES J., GLASNER J.D., RODE C.K., MAYHEW G.F.,

RA GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,

RA MAU B., SHAO Y.;

RT "The complete genome sequence of Escherichia coli K-12.;"

RL SCIENCE 277:1453-1474(1997).

RN [3]

RP SEQUENCE FROM N.A.

RA STRAIN-K12;

RA MEDLINE: 97251357.

RESULT 13

ID GRP2\_ARTSA STANDARD; PRT; 308 AA.

ID P12230;

DT 01-JAN-1990 (REL. 13, CREATED)

DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE GLYCINE RICH PROTEIN GRP33.

OS ARTEMIA SALINA (BRINE SHRIMP).

OC EUARYOTA; METAZOA; ARTHROPODA; CRUSTACEA; BRANCHIOPODA; ANOSTRACA;

OC ARTEMIDI; ARTEMIA.

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE: 88007550.

RA CRUZ-ALVAREZ M., PELICER A.;

RT "Cloning of a full-length complementary DNA for an Artemia salina

RT glycine-rich protein. Structural relationship with RNA binding

RT proteins.;"

RL J. BIOL. CHEM. 262:13377-13380(1987).

CC --!- PTM: TO THE GLY-RICH DOMAIN MIGHT BE METHYLATED.

CC --!- SIMILARITY: TO HD40, THE MAJOR PROTEIN COMPONENT OF ARTEMIA

CC HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN PARTICLES, AND

CC STRUCTURALLY TO OTHER NUCLEAR RNA BINDING PROTEINS.

CC

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CC

DR EMBL: J03453; G161174; -.

DR PIR: A29377; A29379.

FW NUCLEAR PROTEIN; RIBONUCLEOPROTEIN; METHYLATION.

FW DOMAIN 83 118 KH.

FT DOMAIN 186 308 MW; GLY-RICH. CRC32;  
 SQ 308 AA; 33034 MW; 52ADC873 CRC32;

Query Match 14.4%; Score 86; DB 1; Length 308;  
 Best Local Similarity 34.7%; Pred. No. 3. 6.3e+00;  
 Matches 17; Conservative 14; Mismatches 15; Indels 3; Gaps 2;

Db 203 GPMGPGRRGRGRRGGSGPD--RTFDFLEKARMNTSETMPGYYGDES 249  
 Qy 12 GPLGDQLHQALRDLTSSSDELWVILLEKDGMAFQEALDPG-PFDQG 59

RESULT 14  
 ID APE\_PIG STANDARD; PRT; 317 AA.  
 AC P18650; 019099; 01-NOV-1990 (REL. 16, CREATED)  
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)  
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)  
 DE DE  
 GN APOE.  
 OS SUS SCROFA (PIG).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
 ARTIODACTyla; SUIFORMES; SUINA; SUIDE; SUS.  
 RN [1] SEQUENCE FROM N.A.  
 RC TISSUE-LIVER;  
 RA BRZOWSKA A. M., GRIMHOLT U., KULSETH M. A., WOLD I., ROGNE S.;  
 RL SUBMITTED (MAY-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.  
 RN [2] SEQUENCE FROM N.A.  
 RA RAMSOONDA R. J. J., RUCKER E. B., VAZQUEZ J. C., PIEDRAHITA J. A.;  
 RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.  
 RN [3] PRELIMINARY SEQUENCE OF 19-31.  
 RX MIDLINE; 81021043.  
 RA WEISGRABER K. H., TROXLER R. F., RALL S. C., MAHLEY R. W.;  
 RT "Comparison of the human, canine and swine E apoproteins.";  
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 95:374-380(1980).  
 CC -.- FUNCTION: APO-E MEDIATES BINDING, INTERNALIZATION, AND CATABOLISM  
 OF LIPOPROTEIN PARTICLES. IT CAN SERVE AS A LIGAND FOR THE LDL(APO  
 B/E) RECEPTOR AND FOR THE SPECIFIC APO-E RECEPTOR (CHYLOMICRON  
 REMNANT) OF HEPATIC TISSUES.  
 CC -.- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -.- TISSUE SPECIFICITY: SECRETED IN PLASMA.  
 CC -.- SIMILARITY: BELONGS TO THE APOA1 / APOE FAMILY.

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 or send an email to license@isb-sib.ch).

CC  
 DR EMBL; X72835; G311233; -.  
 DR EMBL; U70240; G2388609; -.  
 DR PIR; A05312; A05312.  
 DR PIR; S33450; S33450.  
 DR HSSP; P02649; IOPF.  
 KW GLYCOPROTEIN; PLASMA; LIPID TRANSPORT; HDL; VLDL; CHYLOMICRON;  
 KW HEPARIN-BINDING; REPEAT; SIGNAL.  
 FT SIGNAL 1 18  
 FT CHAIN 19 317  
 FT DOMAIN 157 167  
 FT DOMAIN 161 164  
 FT DOMAIN 228 235  
 FT DOMAIN 79 254  
 FT DOMAIN 79 100  
 FT REPEAT 101 122  
 FT REPEAT 123 144  
 FT REPEAT 145 166  
 FT REPEAT 167 188  
 FT REPEAT 189 210

RESULT 15  
 ID SDOM\_RABBIT STANDARD; PRT; 202 AA.  
 AC P41982;  
 DT 01-NOV-1995 (REL. 32, CREATED)  
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
 DE SUPEROXIDE DISMUTASE [MN] PRECURSOR (EC 1.15.1.1) (FRAGMENT).  
 GN SOD2.  
 OS ORYCTOLAGUS Cuniculus (RABBIT).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
 OC LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.  
 RN [1] SEQUENCE FROM N.A.  
 RC STRAIN-NEW ZEALAND WHITE;  
 RA JACKSON R. M.;  
 RL SUBMITTED (XX-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.  
 CC -.- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE  
 CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.  
 CC -.- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).  
 CC -.- SUBUNIT: HOMOTRIMER (BY SIMILARITY).  
 CC -.- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.  
 CC -.- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE  
 FAMILY.  
 CC  
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 or send an email to license@isb-sib.ch).

CC  
 DR EMBL; L28808; G454175; -.  
 DR PROSITE; PS00088; SOD\_MN; 1.  
 DR PF00081; SodfE; 1.  
 DR HSSP; P04179; IMSD.  
 KW OXIDOPREDUCTASE; MANGANESE; MITOCHONDRION; TRANSIT PEPTIDE.

FT OXIDOPREDUCTASE; MANGANESE; MITOCHONDRION; TRANSIT PEPTIDE.  
 FT NON\_TER 1 1  
 FT TRANSIT <1 5  
 FT CHAIN 5 >202  
 FT METAL 31 31  
 FT METAL 79 79  
 FT METAL 164 164  
 FT METAL 168 168  
 FT NON\_TER 202 202  
 SQ SEQUENCE 202 AA; 22656 MW; 3BFFC2E CRC32;

FT REPEAT 211 232 7.  
 FT REPEAT 233 254 8.  
 FT CONFLICT 35 35 S -> P (IN REF. 2).  
 FT CONFLICT 160 161 NV -> K (IN REF. 2).  
 FT CONFLICT 166 166 V -> L (IN REF. 2).  
 FT CONFLICT 251 252 DE -> E (IN REF. 2).  
 FT CONFLICT 273 273 A -> G (IN REF. 2).  
 FT CONFLICT 275 275 Q -> H (IN REF. 2).  
 FT CONFLICT 277 277 R -> L (IN REF. 2).  
 FT CONFLICT 289 289 M -> I (IN REF. 2).  
 FT CONFLICT 303 303 A -> G (IN REF. 2).  
 SQ SEQUENCE 317 AA; 36599 MW; B791DA99 CRC32;

Query Match 14.4%; Score 86; DB 1; Length 317;  
 Best Local Similarity 28.4%; Pred. No. 3. 6.3e+00;  
 Matches 21; Conservative 21; Mismatches 23; Indels 4; Gaps 3;

Db 54 LRVW QSLISQVQEL - LSTKVQBLTLEIIEKSMKVEYKRELEA QLGIVVTOETAR 109  
 Qy 7 DRIVFGPLGLQHQLRDLTSSSDELWVILLEKDGMAFQEALDPG-PFDQGSPFQEL 66

Db 110 LSKELQQAQARVGA 123  
 Qy 67 LDGQQASPIHPS 80

RA AIBA H., BABA T., FUJITA K., HAYASHI K., INADA T., ISONO K.,  
 RX MEDLINE: 89323435.  
 RA MORIIE L., MORIIE F., ROUX A. F., GODDET J., FORGET B. G., DEMOROY L.,  
 RA GARBARZ M., DHERMY D., KASTALLY R., DELAUNAY J.,  
 RT "Spectrin" Tunis (Sp alpha I/78), an elliptocytogenic variant, is due  
 to the CCG-->GG codon change (Arg-->Trp) at position 35 of the  
 alpha I domain.";  
 RT BLOOD 74:828-832(1989).  
 RL [21]  
 RP VARIANT GENOVA.  
 RX MEDLINE: D4250920.  
 RA PERROTTA S., DEL GIUDICE E. M., ALLOISTO N., SCIARRATTA G., PINTO L.,  
 RA DELAUNAY J., CUTTINO S., LOLASCON A.;  
 RT "Mild elliptocytosis associated with the alpha 34 Arg-->Trp mutation  
 in spectrin Genova (alpha I/74)." ;  
 RL BLOOD 83:3346-3349(1994).  
 RN [22]  
 RP VARIANT ANASTASIA.  
 RX MEDLINE: 93290423.  
 RA PERROTTA S., LOLASCON A., DE ANGELIS F., PAGANO L., COLOMNA G.,  
 RA CUTTINO S., DEL GIUDICE E. M.,  
 RT "Spectrin Anastasia (alpha I/78); a new spectrin variant (alpha 45  
 Arg-->Thr) with moderate elliptocytogenic potential." ;  
 RL PIR: J. HAEMATOL. 89:933-936(1995).  
 CC -!- FUNCTION: SPECTRIN IS THE MAJOR CONSTITUENT OF THE CYTOSKELETAL  
 CC NETWORK UNDERLYING THE ERYTHROCYTE PLASMA MEMBRANE. IT ASSOCIATES  
 CC WITH BAND 4.1 AND ACTIN TO FORM THE CYTOSKELETAL SUPERSTRUCTURE OF  
 CC THE ERYTHROCYTE PLASMA MEMBRANE.  
 . . . . .  
 Note: remainder of annotations omitted.

Query Match 14.7%; Score 88; DB 1; Length 2418;  
 Best Local Similarity 31.3%; Pred. No. 2.0e+00;  
 Matches 15; Conservative 15; Mismatches 15; Indels 3; Gaps 3;  
 ID 1318 AEDLTGIEILLRRH-QHRRADMAEAAPPFQAEQEDFSALIDSGHHSAP 1364  
 DT 01-MAR-1992 (REL. 21, CREATED)  
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE HYPOTHETICAL 20.1 KD PROTEIN IN SELD-SPPA INTERGENIC REGION (ORF183).  
 QY 30 SDELSWIELLERDGMAFQEALDP-GP-FDQGSPFAQEDLLDDGQQASP 75

RESULT 12  
 ID YDJA\_ECOLI STANDARD; PRT; 183 AA.  
 AC P24250;  
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE HYPOTHETICAL 20.1 KD PROTEIN IN SELD-SPPA INTERGENIC REGION (ORF183).  
 QY 30 SDELSWIELLERDGMAFQEALDP-GP-FDQGSPFAQEDLLDDGQQASP 75

Query Match 14.7%; Score 88; DB 1; Length 2418;  
 Best Local Similarity 31.3%; Pred. No. 2.0e+00;  
 Matches 15; Conservative 15; Mismatches 15; Indels 3; Gaps 3;  
 ID 1318 AEDLTGIEILLRRH-QHRRADMAEAAPPFQAEQEDFSALIDSGHHSAP 1364  
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE HYPOTHETICAL 20.1 KD PROTEIN IN SELD-SPPA INTERGENIC REGION (ORF183).  
 QY 30 SDELSWIELLERDGMAFQEALDP-GP-FDQGSPFAQEDLLDDGQQASP 75

RESULT 13  
 ID GR03\_ARTSA STANDARD; PRT; 308 AA.  
 AC P12230;  
 DT 01-JAN-1990 (REL. 13, CREATED)  
 DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE GLUCINE-RICH PROTEIN GRP33.  
 OS ARTEMIA SALINA (BRINE SHRIMP).  
 OC EUKARYOTA; METAZOA; ARTHROPODA; CRUSTACEA; BRANCHIOPODA; ANOSTRACA;  
 ARTEMIDAE; ARTEMIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 9131715.  
 RA SAWERS G., HEIDER J., ZEHELEIN E., BOECK A.,  
 RT "Expression and operon structure of the sel genes of Escherichia coli  
 and identification of a third selenium-containing formate  
 dehydrogenase isoenzyme." ;  
 RT J. BACTERIOL. 173:4983-4993(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAINK12 / MG1655;  
 RX MEDLINE: 9742617.  
 RA BLATTNER F. R., PUNKETT G. III, BLOCH C. A., PERNIA N. T., BURLAND V.,  
 RA GREGORY M., COLLADO-VIDES J., GLASNER J. D., RODE C. K., MAYHEW G. F.,  
 RA GREGOR J., DAVIS N. W., KIRKPATRICK H. A., GOEDEN M. A., ROSE D. J.,  
 RA MAU B., SHAO Y.;  
 RT "The complete genome sequence of Escherichia coli K-12." ;  
 RL SCIENCE 277:1453-1474(1997).  
 RP SEQUENCE FROM N.A.  
 RC STRAINK12.  
 RX MEDLINE: 97251357.

RA AIBA H., BABA T., FUJITA K., HAYASHI K., INADA T., ISONO K.,  
 RA KITAGAWA M., MAKINO K., MIKI T., MIZOURUCHI K., MORI H., MORI T.,  
 RA MOTOMURA K., NAKADE S., NAKAMURA Y., NISHIMOTO H., NISHIO Y.,  
 RA OSHIMA T., SAITO N., SAMPEI G., SEKI Y., SIVASUNDARAM S.,  
 RA TAGAMI H., TAKEDA J., TAKEMOTO K., TAKEUCHI Y., WADA C.,  
 RA YAMAMOTO Y., HORTUCHI T.  
 RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome  
 corresponding to the 28.0-40.1 min region on the linkage map." ;  
 RL DNA RES. 3:363-377(1995).  
 CC -!- SIMILARITY: STRONG, TO H. INFLUENZAE HI1542.  
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 CC ---  
 DR EMBL: M88961; GI47021; -.  
 DR EMBL: A000271; GI78063; -.  
 DR EMBL: D00820; GI742876; -.  
 DR PIR: A40360; A40360.  
 DR ECOGENE: EG1134; YDJA.  
 DR PFAM: PF00881; Nitroreductase; 1.  
 KW HYPOTHETICAL PROTEIN.  
 SQ SEQUENCE 183 AA; 20059 MW; 6909542D CRC32;

Query Match 14.4%; Score 86; DB 1; Length 183;  
 Best Local Similarity 26.9%; Pred. No. 3.63e+00;  
 Matches 14; Conservative 15; Mismatches 20; Indels 3; Gaps 3;  
 ID 20 APTGCEQLQNLIRAGMGRADPKHSKMQPHWPHFVIEGGERFERSAVLQQGATAAGS 71  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE GLUCINE-RICH PROTEIN GRP33.  
 OS ARTEMIA SALINA (BRINE SHRIMP).  
 OC EUKARYOTA; METAZOA; ARTHROPODA; CRUSTACEA; BRANCHIOPODA; ANOSTRACA;  
 ARTEMIDAE; ARTEMIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 8807550.  
 RA CRUZ-ALVAREZ M., PELLICER A.,  
 RT "Cloning of a full-length complementary DNA for an Artemia salina  
 RT glycine-rich protein. Structural relationship with RNA binding  
 RT proteins." ;  
 RL J. BIOL. CHEM. 262:13377-13380(1987).  
 CC -!- PTM: THE ARGININES IN THE GLU-RICH DOMAIN MIGHT BE METHYLATED.  
 CC -!- SIMILARITY: TO HD40, THE MAJOR PROTEIN COMPONENT OF ARTEMIA  
 CC HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN PARTICLES AND  
 CC STRUCTURALLY TO OTHER NUCLEAR RNA BINDING PROTEINS.  
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 CC ---  
 DR EMBL: J03453; GI161174; -.  
 DR PIR: A29379; A29379.  
 KW NUCLEAR PROTEIN; RIBONUCLEOPROTEIN; METHYLATION.  
 FT DOMAIN 83 118 KH.



Tue Oct 26 15:35:01 1999

US-08-978-217-7.rsp

Page 9

Query Match Similarity 14.2%; Score 85; DB 1; Length 202;  
Best Local Similarity 25.0%; Pred. No. 4 82e-00; Matches 13;  
Matches 13; Conservative 16; Mismatches 21; Indels 2; Gaps 2;  
Db 8 SLPIDIPYDGALEPHINAQIMELHHSKHHA-AYVNNNATEEK-YREALARG 57  
Qy 3 ALEELRLVFGPLGDOQLRDLTSSSDELSWIIEELERDGMAFQEALDPG 54

Search completed: Thu Oct 21 16:30:14 1999  
Job time : 29 secs.

